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RAW SEQUENCE LISTING   ·   DATE: 01/24/2003
PATENT APPLICATION: **US/10/080,522**   TIME: 08:46:21

Input Set : **A:\Sequence Listing.txt**
Output Set: **N:\CRF4\01242003\J080522.raw**

SEQUENCE LISTING
```
        4  (1) GENERAL INFORMATION:
        6         (i) APPLICANT: KAUFMAN, RUSSEL E.
        7                        SLENTZ-KESLER, KIMBERLY
        9        (ii) TITLE OF INVENTION: GENE PRODUCT OVER EXPRESSED IN CANCER
       10                                 CELLS
       12       (iii) NUMBER OF SEQUENCES: 2
       14        (iv) CORRESPONDENCE ADDRESS:
       15             (A) ADDRESSEE: NIXON & VANDERHYE P.C.
       16             (B) STREET: 1100 NORTH GLEBE ROAD, 8TH FLOOR
       17             (C) CITY: ARLINGTON
       18             (D) STATE: VIRGINIA
       19             (E) COUNTRY: U.S.A.
       20             (F) ZIP: 22201-4714
       22         (v) COMPUTER READABLE FORM:
       23             (A) MEDIUM TYPE: Floppy disk
       24             (B) COMPUTER: IBM PC compatible
       25             (C) OPERATING SYSTEM: PC-DOS/MS-DOS
       26             (D) SOFTWARE: PatentIn Release #1.0, Version #1.30
       28        (vi) CURRENT APPLICATION DATA:
C-->   29             (A) APPLICATION NUMBER: US/10/080,522
C-->   30             (B) FILING DATE: 25-Feb-2002
W-->   46             (C) CLASSIFICATION:
       43       (vii) PRIOR APPLICATION DATA:
       34             (A) APPLICATION NUMBER: US 09/539,774
       35             (B) FILING DATE: 31-MAR-2000
       39             (A) APPLICATION NUMBER: US 09/210,474
       40             (B) FILING DATE: 14-DEC-1998
       44             (A) APPLICATION NUMBER: US 08/755,559
       45             (B) FILING DATE: 22-NOV-1996
       48      (viii) ATTORNEY/AGENT INFORMATION:
       49             (A) NAME: WILSON, MARY J.
       50             (B) REGISTRATION NUMBER: 32,955
       51             (C) REFERENCE/DOCKET NUMBER: 1579-645
       53        (ix) TELECOMMUNICATION INFORMATION:
       54             (A) TELEPHONE: (703) 816-4000
       55             (B) TELEFAX: (703) 816-4100
       58  (2) INFORMATION FOR SEQ ID NO: 1:
       60         (i) SEQUENCE CHARACTERISTICS:
       61             (A) LENGTH: 248 amino acids
       62             (B) TYPE: amino acid
       63             (C) STRANDEDNESS:
       64             (D) TOPOLOGY: linear
```

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```
66     (ii) MOLECULE TYPE: protein
71     (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:
73     Met Gln Thr Cys Pro Leu Ala Phe Pro Gly His Val Ser Gln Ala Leu
74      1             5                  10                15
76     Gly Thr Leu Leu Phe Leu Ala Ala Ser Leu Ser Ala Gln Asn Glu Gly
77                  20                  25              30
79     Trp Asp Ser Pro Ile Cys Thr Glu Gly Val Val Ser Val Ser Trp Gly
80          35                  40                  45
82     Glu Asn Thr Val Met Ser Cys Asn Ile Ser Asn Ala Phe Ser His Val
83          50                  55                  60
85     Asn Ile Lys Leu Arg Ala His Gly Gln Glu Ser Ala Ile Phe Asn Glu
86      65                  70                  75                80
88     Val Ala Pro Gly Tyr Phe Ser Arg Asp Gly Trp Gln Leu Gln Val Gln
89                  85                  90                  95
91     Gly Gly Val Ala Gln Leu Val Ile Lys Gly Ala Arg Asp Ser His Ala
92                  100                 105                 110
94     Gly Leu Tyr Met Trp His Leu Val Gly His Gln Arg Asn Asn Arg Gln
95                  115                 120                 125
97     Val Thr Leu Glu Val Ser Gly Ala Glu Pro Gln Ser Ala Pro Asp Thr
98          130                 135                 140
100     Gly Phe Trp Pro Val Pro Ala Val Val Thr Ala Val Phe Ile Leu Leu
101     145                 150                 155                160
103     Val Ala Leu Val Met Phe Ala Trp Tyr Arg Cys Arg Cys Ser Gln Gln
104                  165                 170                 175
106     Arg Arg Glu Lys Lys Phe Phe Leu Leu Glu Pro Gln Met Lys Val Ala
107                  180                 185                 190
109     Ala Leu Arg Ala Gly Ala Gln Gln Gly Leu Ser Arg Ala Ser Ala Glu
110                  195                 200                 205
112     Leu Trp Thr Pro Asp Ser Glu Pro Thr Pro Arg Pro Leu Ala Leu Val
113          210                 215                 220
115     Phe Lys Pro Ser Pro Leu Gly Ala Leu Glu Leu Leu Ser Pro Gln Pro
116     225                 230                 235                 240
118     Leu Phe Pro Tyr Ala Ala Asp Pro
119                  245
126 (2)  INFORMATION FOR SEQ ID NO: 2:
128      (i) SEQUENCE CHARACTERISTICS:
129          (A) LENGTH: 2180 base pairs
130          (B) TYPE: nucleic acid
131          (C) STRANDEDNESS: single
132          (D) TOPOLOGY: linear
134      (ii) MOLECULE TYPE: DNA (genomic)
139      (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:
141 ATTCCTGCTT CCTTTAGCGT GAACGCGGGT GCGGTGCCTC CCGTGAAATA ATAAATTCAC      60
143 CGTCACGCTT GTTGTGAACG CGGGTGGTTC CCGAAACTTG GAGGCTTCCC GTAAACCCAG     120
145 CTCCTTCCTC ATCTGGGAGG TGGGTCCCGC GCGGGTCCGC CGCCTCCTCC CTGGCCCCTC     180
147 CCTCTCGTGT CTTTCATTTT CCTGGGGCTC CGGGGCGCGG AGAAGCTGCA TCCCAGAGGA     240
149 GCGCGTCCAG GAGCGGACCC GGGAGTGTTT CAAGAGCCAG TGACAAGGAC CAGGGGCCCA     300
151 AGTCCCACCA GCCATGCAGA CCTGCCCCCT GGCATTCCCT GGCCACGTTT CCCAGGCCCT     360
153 TGGGACCCTC CTGTTTTTGG CTGCCTCCTT GAGTGCTCAG AATGAAGGCT GGGACAGCCC     420
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```
155 CATCTGCACA GAGGGGGTAG TCTCTGTGTC TTGGGGCGAG AACACCGTCA TGTCCTGCAA    480
157 CATCTCCAAC GCCTTCTCCC ATGTCAACAT CAAGCTGCGT GCCCACGGGC AGGAGAGCGC    540
159 CATCTTCAAT GAGGTGGCTC CAGGCTACTT CTCCCGGGAC GGCTGGCAGC TCCAGGTTCA    600
161 GGGAGGCGTG GCACAGCTGG TGATCAAAGG CGCCCGGGAC TCCCATGCTG GGCTGTACAT    660
163 GTGGCACCTC GTGGGACACC AGAGAAATAA CAGACAAGTC ACGCTGGAGG TTTCAGGTGC    720
165 AGAACCCCAG TCCGCCCCTG ACACTGGGTT CTGGCCTGTG CCAGCGGTGG TCACTGCTGT    780
167 CTTCATCCTC TTGGTCGCTC TGGTCATGTT CGCCTGGTAC AGGTGCCGCT GTTCCCAGCA    840
169 ACGCCGGGAG AAGAAGTTCT TCCTCCTAGA ACCCCAGATG AAGGTCGCAG CCCTCAGAGC    900
171 GGGAGCCCAG CAGGGCCTGA GCAGAGCCTC CGCTGAACTG TGGACCCCAG ACTCCGAGCC    960
173 CACCCCAAGG CCGCTGGCAC TGGTGTTCAA ACCCTCACCA CTTGGAGCCC TGGAGCTGCT   1020
175 GTCCCCCCCA ACCCTTGTTT CCATATGCCG CAGACCCATA GCCGCCTGCA AGGCAGAGAG   1080
177 GACACAGGAG AGCCAGCCCT GAGTGCCGAC CTTGGGTGGC GGGGCCTGGG TCTCTCGTCC   1140
179 CACCCGGAGG GCACAGACAC CGGCTTGCTT GGCAGGCTGG GCCTCTGTGT CACCCACTCC   1200
182 TGGGTGCGTG CAGACCCTTC CCCTCCACCC CCAGGTCTT CCAAGCTCTG CTTCCTCAGT   1260
184 TTCCAAAATG GAACCACCTC ACCTCCGCAG CACCCGACTT ACCAGGACGC ATGCCCCTCC   1320
186 CTCTGCCCTC ATCAAACCCA CAGACCCGGA CTCCCTTTCT GCCACCCCAG GCTGGTCCGG   1380
188 CCCCAGGTGT GGGGTCCGCT CTCTCCACTC CCAGGGCTCC GCGCCCAAGT GAGGGGGCCC   1440
190 CTGCCGGAGC CTCAGACACA CTGGAGTTCA GGGCTGGGGG GGCCTTGGCA CATACCTGTC   1500
192 CCTTGGCTAT GAGCAGGCTT TGGGGGCCCT TCCGCGGCAG CCCCGGGGGC CGAGGTAGGG   1560
194 TCTGGGGGCT TAGAGGCTGG GATGGCTCCT GGCCCCACCG CCAGGGGGCA AGCGCAGGCC   1620
196 GGGCTGGGAG GCGGCGGCGG CGGCTCGGGC TGGGGGGTCA GGTGGACGCT GCCTCCGGGG   1680
198 CTGGTCGCGC ATCCCTCAGT CCCTCGGCCA CCCGGGGGTC GCTCCCTCGT GCCCACCGCA   1740
200 CCTGCCGAGC CTCTTTGGAC CCAGATCTGT TCATGCTTTT GTCTTCGTCA CTGCGGCGGG   1800
202 GCCCTTTGAT GTCTTCATCT GTATGGGGTG GAAAAATCAC CGGGAATCCC CCTTCAGTTC   1860
204 TTTGAAAAAG TTCCATGACT CGAATATCTG AAATGAAGAA AACAAACCGA CTCACAAACC   1920
206 TCCAAGTAGC TCCAAATGCA ATTTTTAAAA TGGAAAACAA AAATCTGAAA GAAACGTCTT   1980
208 TAGTGGCTTT AAGCCCCAAA ACGTCCCTAA GGCGTCCTCG AGATGAAGAC GGGGGGGAGC   2040
210 CCCAGCCAGG TGGAGACCCC GCAGGACGCG GCGGCGCCCG GTGACCGAGG CCTCGCACAG   2100
212 CCGGCCGCCC TGAGGGTCGG GCCGAGCCAG GGTCCAAGAG GGGCGCGTTT GTGTCTCGGG   2160
214 TTAAAATAAG GTTCCGTCCG                                                2180
```

VERIFICATION SUMMARY
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Output Set: **N:\CRF4\01242003\J080522.raw**

```
L:29 M:220 C: Keyword misspelled or invalid format, [(A) APPLICATION NUMBER:]
L:30 M:220 C: Keyword misspelled or invalid format, [(B) FILING DATE:]
L:36 M:238 W: Alpha Fields not Ordered, Reordered [(C) CLASSIFICATION:] of (1)(vi)
L:41 M:238 W: Alpha Fields not Ordered, Reordered [(C) CLASSIFICATION:] of (1)(vi)
L:46 M:238 W: Alpha Fields not Ordered, Reordered [(C) CLASSIFICATION:] of (1)(vi)
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